

FIGURE 1

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LyP1/2	MDOREILOKF LDEAQSKKIT KEEFANEFLK LKRQSTKYKA DKIYPTTVAE	50
PEP	MDOREILOQL LKEAQKKKLN SEEFASEFLK LKRQSTKYKA DKIYPTTVAQ	50
Consensus	MDOREILOQ.. L.EAQ.KK.. .EEFA.EFLK LKRQSTKYKA DK.YPTTVA.	50
LyP1/2	NAKNIKKNRY KDILPYDYSR VELSLITSDE DSSYINANFI KGVYGPKAYI	100
PEP	RPKNIKKNRY KDILPYDHSL VELSLITSDE DSSYINASFI KGVYGPKAYI	100
Consensus	..KNIKKNRY KDILPYD.S. VELSL.TSDE DSSYINA.FI KGVYGPKAYI	100
LyP1/2	ATOGPLSTTL LDFWRMIWEY SVLIVMACM EYEMGKKCE RYWAEPGEMQ	150
PEP	ATOGPLSTTL LDFWRMIWEY RILVIVMACM EFEMGKKCE RYWAEPGETQ	150
Consensus	ATOGPLSTTL LDFWRMIWEY ..L.IVMACM E.EMGKKCE RYWAEPGE.Q	150
LyP1/2	LEFGPFSVSC EAEKRKSDYI IRTLKVKFNS ETRTIYQFHY KNWPDHDVPS	200
PEP	LQFGPFSISC EAEKKKSDYK IRTLKAKFNN ETRIIYQFHY KNWPDHDVPS	200
Consensus	L.FGPFS.SC EAEK.KSDY. IRTLK.KFN. ETR.IYQFHY KNWPDHDVPS	200
LyP1/2	SIDPILELIW DVRCYQEDDS VPICIHCSAG CGRTGVICAI VDYTWMLKD	250
PEP	SIDPILQLIW DMRCYQEDDC VPICIHCSAG CGRTGVICAV -DYTWMLKD	249
Consensus	SIDPIL.LIW D.RCYQEDD. VPICIHCSAG CGRTGVICA. .DYTWMLKD	250
LyP1/2	GIIPENFSVF SLIREMRTQR PSLVQTQEQQY ELVYNAV LEL FKRQMDVIRD	300
PEP	GIIPKNFSVF NLIQEMRTQR PSLVQTQEQQY ELVYS AV LEL FKRHMDVISD	299
Consensus	GIIP.NFSVF .LI.EMRTQR PSLVQTQEQQY ELVY.AV LEL FKR.MDVI.D	300
LyP1/2	KHSGTESQAK HClPEKNHTL QADSYSPLNP KSTTKAAKMM NQQR---TKM	347
PEP	NHLGREIQAQ CSIEPQLSLTV EADSCPLDLP KNAMRDVKTT NQHSKOGAEA	349
Consensus	.H.G.E.QA. ..IPE...T. .ADS....LP K.....K.. NQ.....	350
LyP1/2	EIKESSSFDF RTSEISAKEE LVLHPAKSST SFDFLELNYS FDKNADTTMK	397
PEP	ESTGGSSLGL RTSTMNAEEE LVLHSAKSSP SFNCLELNCG CNNKAVITRN	399
Consensus	E....SS... RTS...A.EE LVLH.AKSS. SF..LELN..A..T..	400

FIGURE 2

LyP1:2	WQTKAFFPIVG EPLQKHOQLD LGSLLFEGCS NSKPVNAAGR YFNSKVPITR	447
PEP	GQARASPVVG EPLQKYQSLD FGSMILFGSCP SALPINTADR YHNSKGPVKR	449
Consensus	.Q..A.P.VG EPLQK.QSLD .GS.LF..C. ...P.N.A.R Y.NSK.P..R	450
LyP1:2	TKSTPFELIQ QRETKEVDSK ENFSYLESQP HDS-CFVEMQ AQKVMHVSSA	496
PEP	TKSTPFELIQ QRKTNDLAVG DGFSCLESQH HEHYSLRELQ VQRVAHVSS	499
Consensus	TKSTPFELIQ QR.T..... .FS.LESQ. H.....E.Q .Q.V.HVSS.	500
LyP1:2	ELNYSLPYDS KHQIRNASNV KHHDSALGV YSYIPLVNP YFSSWPPSGT	546
PEP	ELNYSLPGAC ----DASCV PRHSPGALRV HLYTSLAEDP YFSSSPPNSA	544
Consensus	ELNYSLP...AS.V . .H...AL.V . .Y..L.E.P YFSS.PP...	550
LyP1:2	SSKMSLDLPE KQDGTVFPSS LLPSTSLSF SYYNSHNSLS LNSPTNISSL	596
PEP	DSKMSFDLPE KQDGATSPGA LLPASSTTSF FYSNPHDSLV MNTLTSFSPP	594
Consensus	.SKMS.DLPE KQDG...P.. LLP.SST..F .Y.N.H.SL. .N..T..S..	600
LyP1:2	LNQESAVLAT APRIDDEIPP PLPVRTPESF IVVEEAGEFS PNVPKSLSSA	646
PEP	LNQETAVEAP SRRTDDEIPP PLPERTPESF IVVEEAGEPS PRVTESL--P	642
Consensus	LNQE.AV.A. . .R.DDEIPP PLP.RTPESF IVVEEAGE.S P.V..SL...	650
LyP1:2	VVKVIGTSLE WGGTSEPKKF DDSVILRPSK SVKLRSPKSE LHQDRSSPPP	696
PEP	LVVTFGASPE CSGTSEMKS- HDSVGFTPSK NVKLRSPKSD RHQDGSP-PP	690
Consensus	.V..G.S.E ..GTSE.K.. .DSV...PSK .VKLRSPKS. .HOD.S..PP	700
LyP1	***** PLPERTLESF FLADEDCMQA QSIETYSTS PDMENSTSS KQTLKTPGKS	746
PEP	PLPERTLESF FLADEDCIQA QAVQTSSTS PETTENSTSS KQTLRTPGKS	740
Consensus	PLPERTLESF FLADEDC.QA Q...T.STSY P.T.ENSTSS KQTL.TPGKS	750
LyP1	FTRSKSLKIL RNMKKSICNS CPPNPKAESV QSNNSSSFLN FGFANRFSP*	796
PEP	FTRSKSLKIF RNMKKSVCNS SSPSKPTERV QPKNNSSFLN FGFGNRFSP	790
Consensus	FTRSKSLKI. RNMKKS.CNS ..P.KP.E.V Q..NSSSFLN FGF.NRFSP	800
LyP1	***** KGPRNPPPTW NI	808
PEP	KGPRNPPSAW NM	802
Consensus	KGPRNPP..W N.	

↓ LyP2
GKNFSW L 692

FIGURE 2 CONT'D

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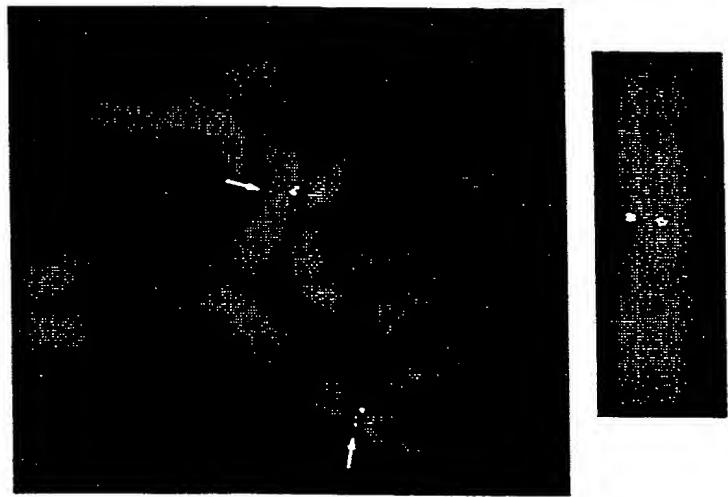


FIGURE 3A

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Chromosome 1

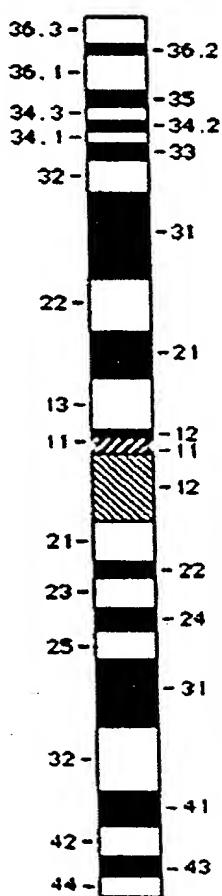


FIGURE 3B

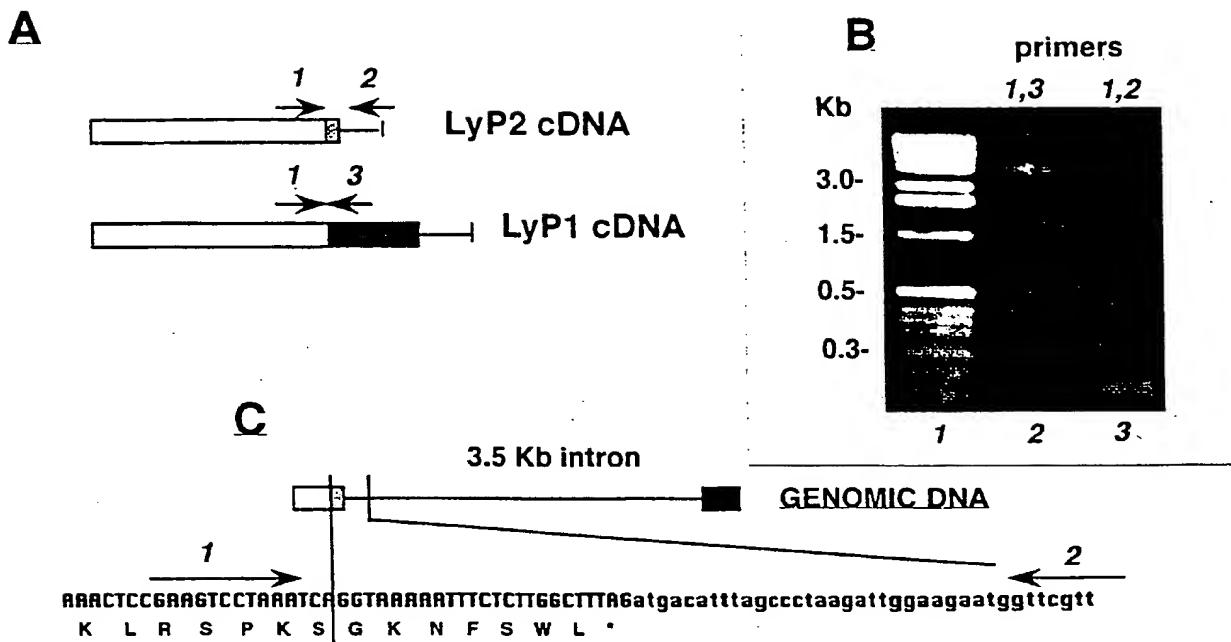


FIGURE 4

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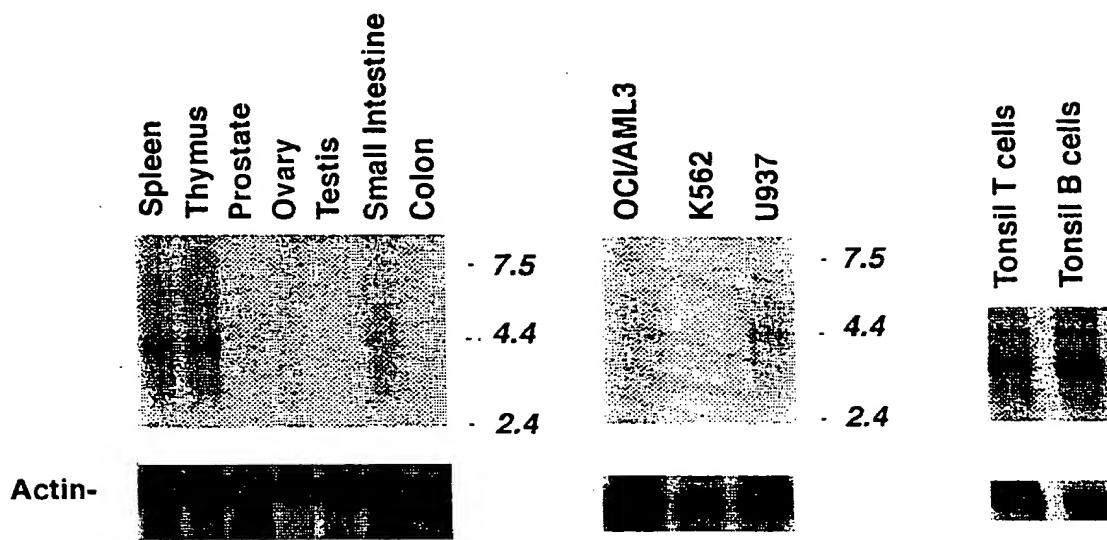


FIGURE 5A

FIGURE 5B

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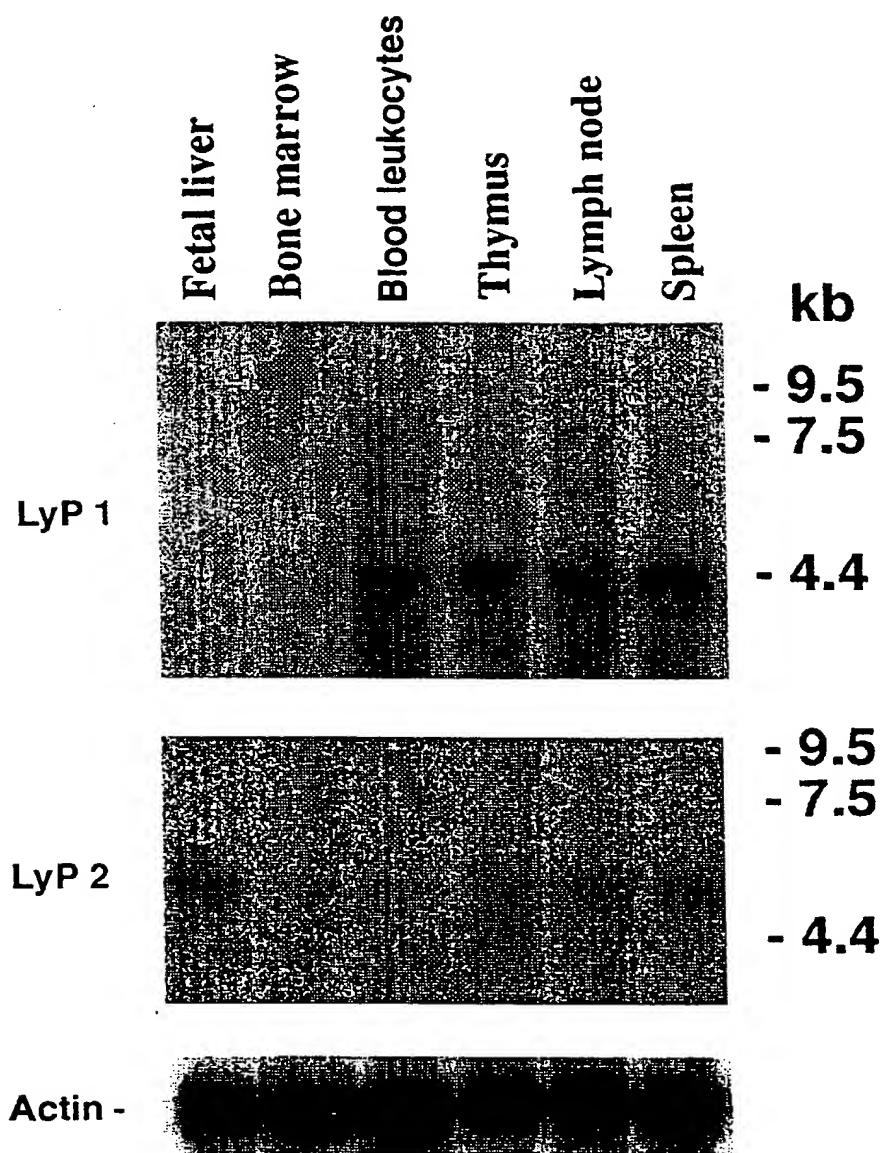


FIGURE 5C

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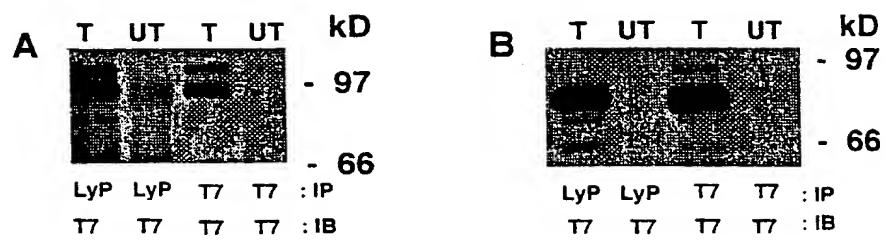


FIGURE 6

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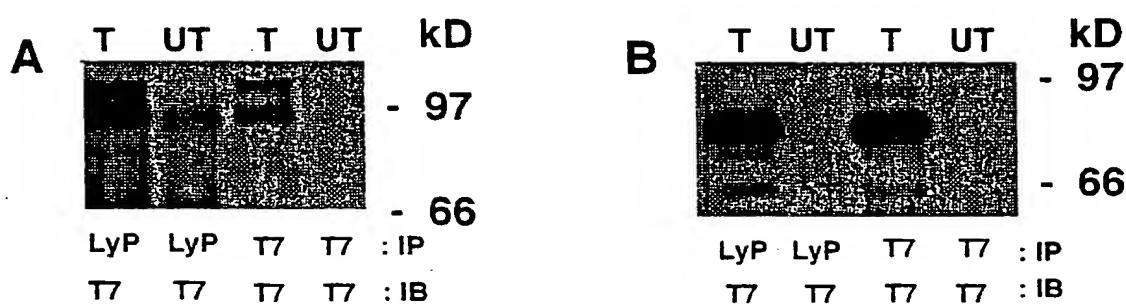


FIGURE 7

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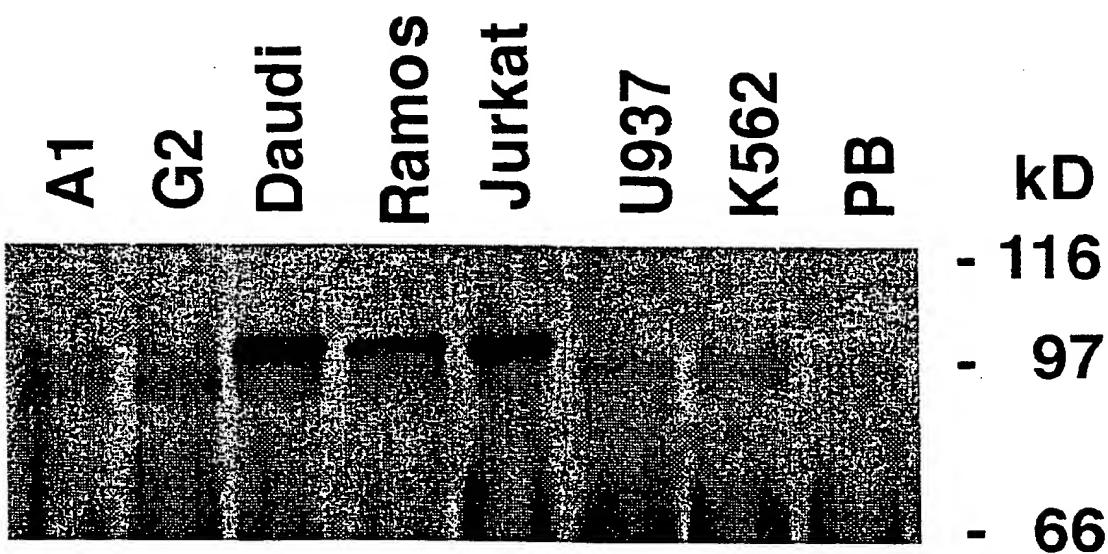


FIGURE 8

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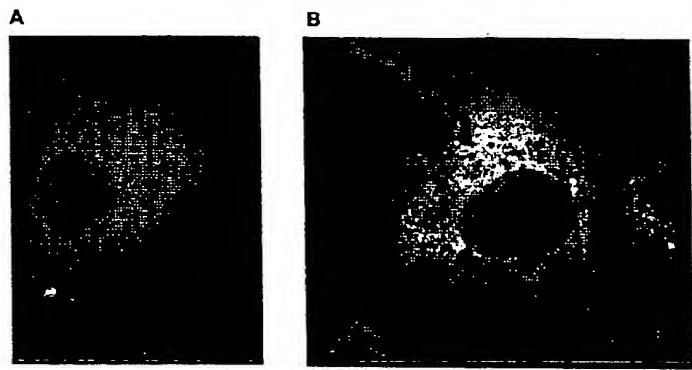


FIGURE 9

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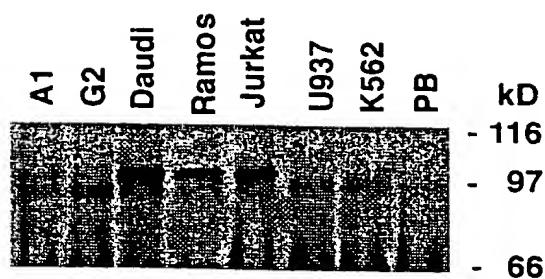


FIGURE 10

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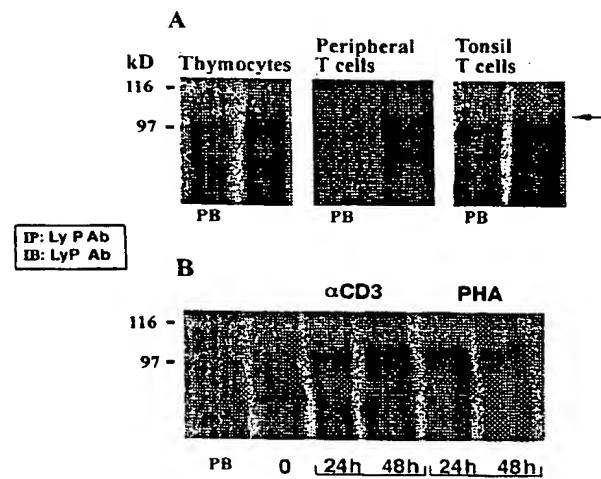


FIGURE 11

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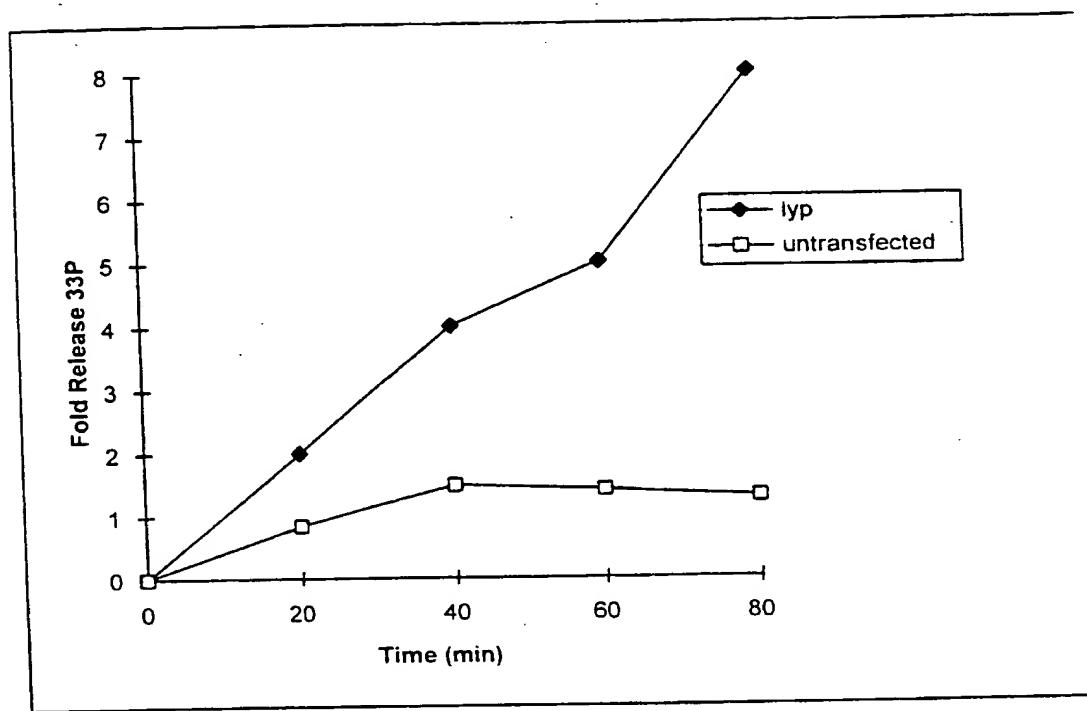


FIGURE 12

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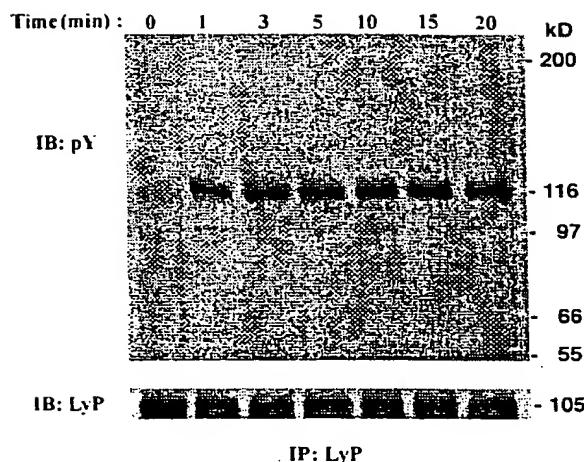
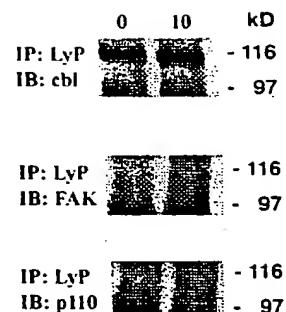
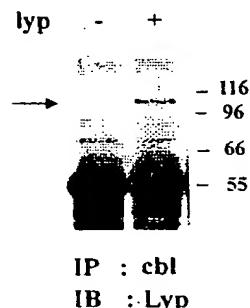
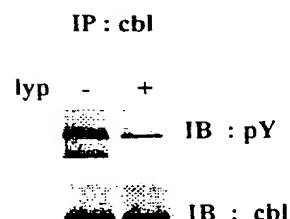
A**B****C****D**

FIGURE 13

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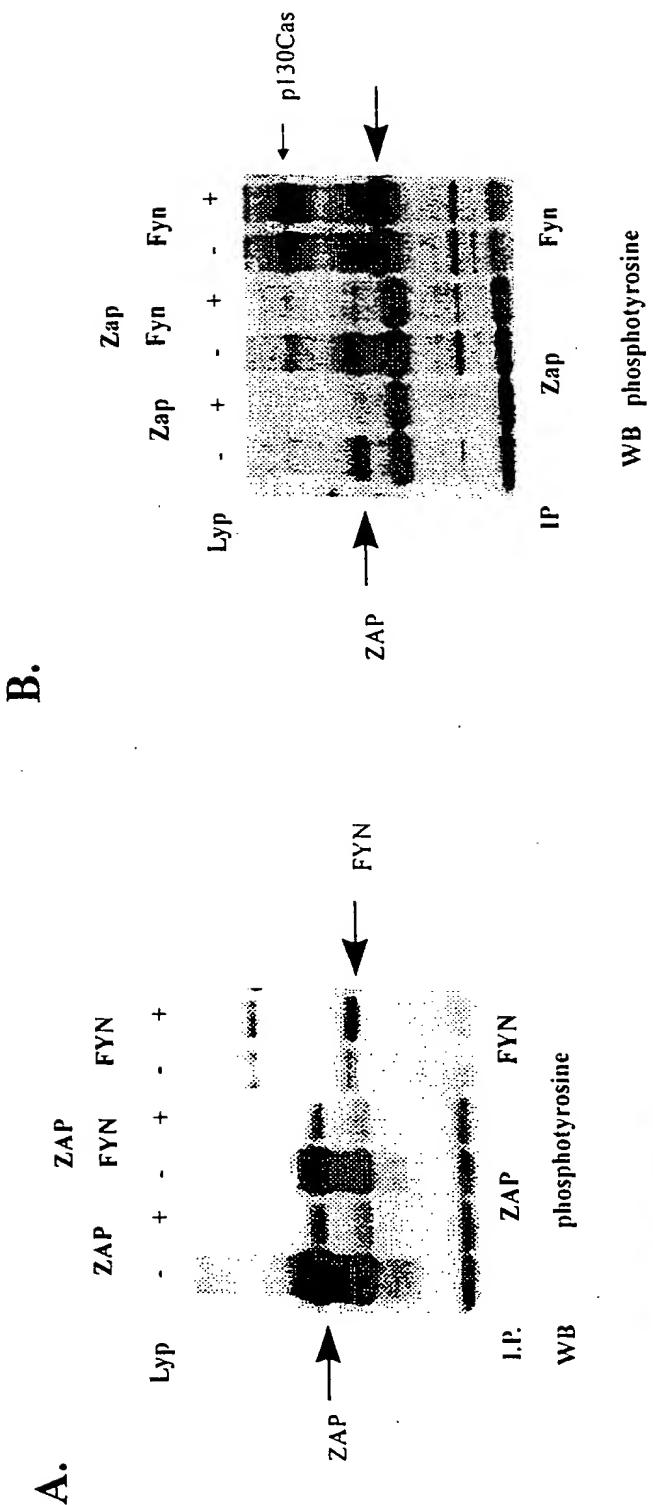


FIGURE 14

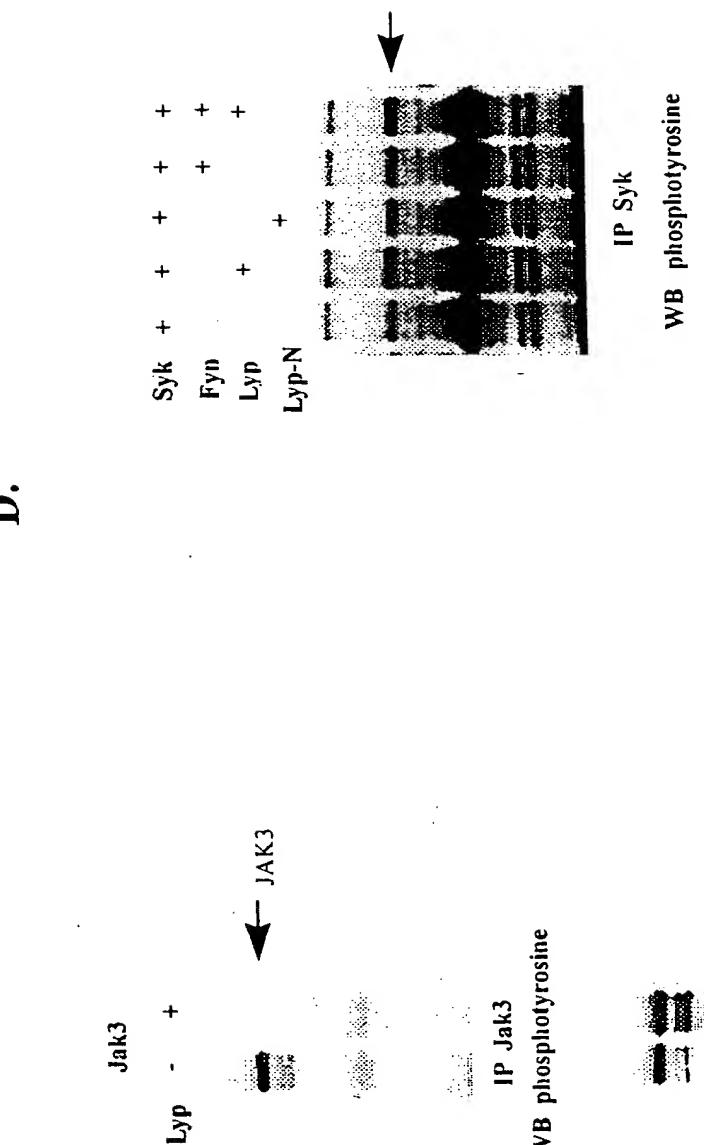


FIGURE 15